



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 129514

TO: Cynthia Wilder
Location: 2a35 / 2c18
Sunday, August 15, 2004
Art Unit: 1637
Phone: 272-0791
Serial Number: 10 / 082830

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1A51
Phone: 272-2504

jan.delaval@uspto.gov

Search Notes

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L2 ANSWER 3 OF 3 GENBANK® COPYRIGHT 2004 on STN

LOCUS (LOC): **AL139327** GenBank (R)
GenBank ACC. NO. (GBN): **AL139327**
GenBank VERSION (VER): AL139327.18 GI:9187183
CAS REGISTRY NO. (RN): 256602-08-1
SEQUENCE LENGTH (SQL): 149559
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 4 Oct 2000
DEFINITION (DEF): Human DNA sequence from clone RP11-408E5 on chromosome 13q11-12.2 Contains an FSH primary response homolog 1 (FSHPRH1) pseudogene, two genes for novel proteins, a gene for an orthologue of mouse tubulin alpha 3 (TUBA3) or 7 (TUBA7) and a gene for a novel protein similar to DMPK-like CDC42-binding protein kinase beta (CDC42BPB). Contains ESTs, STSs and GSSs, complete sequence.

SOURCE: human.
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo

NUCLEIC ACID COUNT (NA): 44987 a 32382 c 32028 g 40162 t

COMMENT:

On Jul 14, 2000 this sequence version replaced gi:8573820. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13

Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr13>

RP11-408E5 is from the library RPCI-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/>

VECTOR: pBACe3.6

This sequence is the entire insert of clone RP11-408E5 The true left end of clone RP11-385E5 is at 130453 in this sequence.

REFERENCE: 1 (bases 1 to 149559)
AUTHOR (AU): Blakey,S.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (04-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

FEATURES (FEAT):
Feature Key Location Qualifier

source	1..149559	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="13" /map="q11-12.2" /clone="RP11-408E5" /clone-lib="RPCI-11.2"
misc-feature	1..162	/note="match: GSS: Em:AQ149744"
gene	join(2..159,967..1064, 2174..2265,4440..4557, 4640..4731, 12560..12759)	/gene="bA408E5.1"
CDS	join(2..159,967..1064, 2174..2265,4440..4557, 4640..4731, 12560..12759)	/gene="bA408E5.1" /note="bA408E5.1 (FSH primary response homolog 1 (FSHPRH1) pseudogene) match: cDNAs: Em:X97249 Em:X90355 match: ESTs: Em:AA936257 Em:M78295 match: proteins: Sw:Q92674 Sw:Q63517" /codon-start=1 /pseudo /evidence=not-experimental
misc-feature	7..657	/gene="bA408E5.1" /note="match: GSS: Em:AQ742652"
misc-feature	11..405	/gene="bA408E5.1" /note="match: GSS: Em:AQ829597"
misc-feature	19..404	/gene="bA408E5.1" /note="match: GSS: Em:AQ742653"
repeat-region	217..382	/note="FRAM repeat: matches -7..165 of consensus"
repeat-region	399..690	/note="AluSx repeat: matches 1..291 of consensus"
repeat-region	691..748	/note="29 copies 2 mer tg 79% conserved"
repeat-region	693..756	/note="4 copies 16 mer 79% conserved"
repeat-region	786..879	/note="AluJ/FLAM repeat: matches 1..94 of consensus"
repeat-region	1252..1299	/note="3 copies 16 mer 91% conserved"
misc-feature	complement(1480..1954)	/note="match: GSS: Em:AQ564652"
misc-feature	2003..2361	/gene="bA408E5.1" /note="match: GSS: Em:B84641"
repeat-region	2346..2637	/note="AluJo repeat: matches 1..298 of consensus"
repeat-region	2946..3153	/note="L2 repeat: matches 2424..2634 of consensus"
repeat-region	3196..3522	/note="AluJb repeat: matches 1..309 of consensus"
repeat-region	3623..3958	/note="L2 repeat: matches 1519..1874 of consensus"
repeat-region	5139..5433	/note="AluJo repeat: matches 1..295 of consensus"
repeat-region	6199..6503	/note="AluSx repeat: matches 1..304 of consensus"
repeat-region	6546..6837	/note="AluSq repeat: matches 1..294 of consensus"
repeat-region	6892..7182	/note="AluJb repeat: matches 3..293 of consensus"
repeat-region	7189..7365	/note="AluSg/x repeat: matches 125..303 of consensus"

repeat-region	7507..7777	/note="AluSx repeat: matches 6..278 of consensus"
repeat-region	8074..8244	/note="MER5A repeat: matches 3..189 of consensus"
repeat-region	8327..8606	/note="AluJo repeat: matches 1..289 of consensus"
misc-feature	8883..8997	/gene="bA408E5.1"
repeat-region	9328..9608	/note="match: GSS: Em:AQ549314"
repeat-region	10038..10071	/note="AluSx repeat: matches 17..297 of consensus"
misc-feature	complement(10073..10532)	/note="17 copies 2 mer ta 85% conserved"
repeat-region	10178..10488	/note="match: GSS: Em:AQ409701"
repeat-region	10178..10488	/note="AluSx repeat: matches 1..306 of consensus"
repeat-region	11655..11953	/note="AluSq repeat: matches 1..301 of consensus"
repeat-region	11958..12250	/note="AluJb repeat: matches 1..297 of consensus"
repeat-region	13190..13267	/note="MADE1 repeat: matches 3..80 of consensus"
misc-feature	13417..13730	/note="match: GSS: Em:AQ725326"
misc-feature	13417..13643	/note="match: GSS: Em:AQ343055 Em:B86062"
repeat-region	13452..13719	/note="L2 repeat: matches 1738..1999 of consensus"
misc-feature	13647..14017	/note="match: GSS: Em:AQ882434"
misc-feature	13650..13881	/note="match: GSS: Em:AQ343055"
repeat-region	14205..14420	/note="L2 repeat: matches 2241..2443 of consensus"
repeat-region	14421..14726	/note="AluJo repeat: matches 1..298 of consensus"
repeat-region	14728..14990	/note="AluJb repeat: matches 1..295 of consensus"
repeat-region	14991..15189	/note="L2 repeat: matches 2443..2693 of consensus"
repeat-region	15190..15326	/note="FLAM-C repeat: matches 1..133 of consensus"
repeat-region	15327..15388	/note="L2 repeat: matches 2693..2750 of consensus"
repeat-region	15509..15828	/note="L2 repeat: matches 1137..1452 of consensus"
repeat-region	16130..16190	/note="U6 repeat: matches 1..61 of consensus"
repeat-region	16298..16583	/note="AluJo repeat: matches 14..299 of consensus"
repeat-region	16616..16910	/note="AluJb repeat: matches 1..288 of consensus"
repeat-region	16976..17274	/note="AluY repeat: matches 1..297 of consensus"
repeat-region	17616..17832	/note="AluJo repeat: matches 82..301 of consensus"
repeat-region	18316..18395	/note="FLAM-C repeat: matches 64..143 of consensus"
repeat-region	18834..19130	/note="AluSg repeat: matches 5..295 of consensus"
repeat-region	19273..19794	/note="L1MB8 repeat: matches 4981..5500 of consensus"
repeat-region	19795..20072	/note="AluSg repeat: matches 2..294 of consensus"
repeat-region	20073..20479	/note="L1MB8 repeat: matches 5500..5931 of consensus"
repeat-region	20480..20777	/note="AluSg repeat: matches

[illegible]

	43495..43601, 43971..44046, 44200..44342))	
polyA-signal	complement(24427..24432	/gene="bA408E5.2"
)	
repeat-region	27997..28100	/note="MIR repeat: matches 61..165 of consensus"
repeat-region	29118..29402	/note="AluJo repeat: matches 3..287 of consensus"
repeat-region	29985..30284	/note="AluJo repeat: matches 1..296 of consensus"
repeat-region	30350..30653	/note="AluSx repeat: matches 1..303 of consensus"
repeat-region	34111..34207	/note="MER5A repeat: matches 8..107 of consensus"
repeat-region	35277..35627	/note="L1M4 repeat: matches 4845..5205 of consensus"
repeat-region	35632..35916	/note="AluJo repeat: matches 4..299 of consensus"
repeat-region	35919..36186	/note="L1MB2 repeat: matches 5733..5995 of consensus"
repeat-region	36205..36340	/note="FLAM-C repeat: matches 3..133 of consensus"
repeat-region	36349..36475	/note="L1MB2 repeat: matches 6030..6151 of consensus"
repeat-region	36507..36659	/note="AluSx repeat: matches 1..154 of consensus"
repeat-region	36660..37736	/note="MER11C repeat: matches 1..1071 of consensus"
repeat-region	37737..37868	/note="AluSx repeat: matches 154..285 of consensus"
repeat-region	38753..39059	/note="AluSx repeat: matches 5..312 of consensus"
repeat-region	39254..39536	/note="L1MC4 repeat: matches 6861..7141 of consensus"
repeat-region	39544..39673	/note="AluJo/FLAM repeat: matches 1..130 of consensus"
repeat-region	39677..39883	/note="AluJo repeat: matches 88..311 of consensus"
repeat-region	39896..40186	/note="AluSx repeat: matches 1..298 of consensus"
repeat-region	40634..40855	/note="L1MC4 repeat: matches 7696..7906 of consensus"
repeat-region	40856..41153	/note="AluJo repeat: matches 7..306 of consensus"
repeat-region	41154..41213	/note="L1MC4 repeat: matches 7906..7967 of consensus"
repeat-region	41227..41493	/note="AluJo repeat: matches 1..290 of consensus"
repeat-region	41504..41804	/note="AluSx repeat: matches 1..297 of consensus"
repeat-region	41811..42098	/note="AluJo repeat: matches 1..302 of consensus"
repeat-region	42099..42393	/note="AluSx repeat: matches 1..286 of consensus"
repeat-region	42394..42525	/note="66 copies 2 mer aa 58% conserved"
misc-feature	complement(43667..44021	/gene="bA408E5.2"
)	
		/note="match: GSS: Em:AQ236055"
repeat-region	44639..44702	/note="32 copies 2 mer aa 73% conserved"
repeat-region	44711..44789	/note="AluJb repeat: matches 210..288 of consensus"

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repeat-region    44790..44930      /note="LTR42 repeat: matches
                                     1..146 of consensus"
mRNA             complement(join(46918.. /gene="bA408E5.3"
47307,50075..50755,
51394..51542,
52489..>52711))

                                     /note="match: cDNAs: Em:M13441
Em:X04757 Em:M12252 Em:Z31591
Em:X66973 Em:M16030 Em:V00388
Em:V01227 Em:Z31585 Em:X71980
Em:X07046 Em:AF081484 Em:M13442
Em:M13443 Em:M13444 Em:M13445
Em:M13446 Em:J00912 Em:AF029250
Em:M12329 Em:AF141923 Em:AF052694
Em:M36623 Em:AF184595 Em:L11645
match: ESTs: Em:AA540629
Em:AA264456 Em:AA498240
Em:AA498095 Em:AU004459
Em:AI614165 Em:AI615312
Em:AA224537 Em:AW077249
Em:AA118405 Em:AA492758
Em:AA264161 Em:AA061327
Em:AI322779 Em:AA146327
Em:AI519618 Em:AA497708
Em:AA144762 Em:AA106749
Em:AA949696 Em:AU005689
Em:AI390044 Em:AA183966
Em:AI239151 Em:AA183735
Em:AA138935 Em:AA144738
Em:AA436991 Em:AA440269
Em:AA263629 Em:AA940785
Em:AA816814 Em:AA263714
Em:AA263783 Em:AW321433 Em:C77779
Em:AA492799 Em:AL042663
Em:AA977217 Em:AI326062
Em:AI000062 Em:AA709190
Em:AA412719 Em:AA402139
Em:AI208021 Em:AA144835
Em:AA581066 Em:AA183761
Em:AA364293 Em:AA174102
Em:AU050296 Em:AA207695
Em:AI187362 Em:AI650384 Em:H03141
Em:AI507603 Em:W30215 Em:N41353
Em:AI028577 Em:W39454 Em:H42101
Em:AA109198 Em:C88532 Em:W34200
Em:AI528779 Em:AA328434
Em:AA930515 Em:AA075054
Em:AA522217 Em:F35549 Em:C82663
Em:AI208775 Em:AI205604
Em:AI608910 Em:AA426374
Em:AI671144 Em:AA081945
Em:AI326064 Em:AA073369
Em:AA499425 Em:AA064557
Em:AA435720 Em:AA124703
Em:AA626698 Em:C03867 Em:AI207994
Em:AA770436 Em:AI016802 Em:C15650
Em:AA333681 Em:AA972117
Em:AI208058 Em:AI353181
Em:AA058000 Em:AI684520
Em:AW589708 Em:AA750509
Em:AU065700 Em:AA397983 Em:F25814
Em:AA425384 Em:H59275 Em:R35502
Em:T19364 Em:AA864072 Em:T51421
Em:AA100343 Em:C02960 Em:AA566384

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Em:C03050 Em:AA403746 Em:H83058
Em:W70952 Em:AA030759 Em:AA008156
Em:T31971 Em:W89546 Em:C04130
Em:AL044269 Em:AL134889
Em:AA275085"
/product="bA408E5.3 (novel protein
(orthologue of mouse tubulin alpha
3 (TUBA3) or 7 (TUBA7)))"
/evidence=not-experimental
gene complement(46918..52711 /gene="bA408E5.3"
)
polyA-site complement(46918) /gene="bA408E5.3"
polyA-site complement(46920) /gene="bA408E5.3"
polyA-signal complement(46938..46943 /gene="bA408E5.3"
)
misc-feature 47007..47309 /note="match: GSS: Em:AQ185244"
CDS complement(join(47011.. /gene="bA408E5.3"
47307,50075..50755,
51394..51542,
52489..>52711))
/note="match: proteins: Sw:P18258
Sw:P41383 Sw:P52273 Sw:P18288
Sw:P05214 Sw:P02551 Tr:O76659
Sw:P06603 Sw:P06605 Sw:P05213
Tr:O61359 Sw:P18241 Tr:O23350
Sw:Q91060 Tr:Q20221 Tr:O44024
Sw:Q25008 Sw:P36220 Sw:Q94570
Tr:Q91831 Tr:Q9UVR1 Sw:P06606
Sw:P30436 Tr:P91910 Tr:Q43606
Tr:Q9STM8 Sw:P12456 Tr:Q9VR13
Tr:Q9VRX3 Tr:Q94586 Sw:Q17299
Tr:Q9Y4T7 Sw:P50719 Tr:Q9ZTL4
Sw:P05218 Sw:P33625 Sw:P09244
Sw:P30157 Sw:P05209 Sw:P30156
Sw:P31017 Tr:Q26234 Tr:Q26233
Tr:Q9YHT7 Tr:Q29220 Tr:O22635
Tr:Q9VED6 Tr:Q19490 Sw:P41742
Tr:O01941 Tr:O01942 Sw:P52274
Sw:P41385 Sw:P49741 Sw:P41387"
/codon-start=1
/evidence=not-experimental
/product="bA408E5.3 (novel protein
(orthologue of mouse tubulin alpha
3 (TUBA3) or 7 (TUBA7)))"
/protein-id="CAC12714.1"
/db-xref="GI:10697001"
/translation="RECISIHVGQAGVQIGNACW
ELYCLEHGIQPDGQMPSDKTIGGG
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ARGHYTIGKEIVDLVLDRIKRLADLCTGLQGFLI
FHSFGGGTGS GFASLLMERLSVDY
GKKSKLEFAIYPAPQVSTAVVEPYNSILTHTTTL
EHSDCAFMVDNEAIYDICRRNLDI
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KTKRTIQFVDWCPTGFKVGINYQPPTVVPGGDLA
KVQRAVCMLSNTTAIAEAWARLDH
KFDLMYAKRAVFVHWYVGEGMEEGEFSEAREDLAA
LEKDYEEVGVDSEAEAEEGEEY"
misc-feature complement(47017..47136 /gene="bA408E5.3"
)

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misc-feature	complement(47204..47309)	/note="match: GSS: Em:AL257635" /gene="bA408E5.3"
misc-feature	47338..47729	/note="match: GSS: Em:AQ419383"
repeat-region	47481..47580	/note="match: GSS: Em:AQ078654"
repeat-region	47836..48108	/note="AluJ/FLAM repeat: matches 2..101 of consensus"
repeat-region	48115..48429	/note="AluJb repeat: matches 4..289 of consensus"
repeat-region	48751..48894	/note="AluY repeat: matches 1..311 of consensus"
repeat-region	48751..48894	/note="MER58A repeat: matches 42..196 of consensus"
repeat-region	48895..49186	/note="AluSx repeat: matches 5..297 of consensus"
repeat-region	49212..49281	/note="AluJ/FRAM repeat: matches 227..297 of consensus"
repeat-region	49285..49538	/note="AluSx repeat: matches 1..257 of consensus"
repeat-region	49620..49903	/note="AluSx repeat: matches 1..312 of consensus"
misc-feature	complement(50026..50341)	/gene="bA408E5.3"
misc-feature	complement(50026..50351)	/note="match: GSS: Em:AZ042582" /gene="bA408E5.3"
misc-feature	50073..50650	/note="match: GSS: Em:AZ078821"
repeat-region	50995..51293	/note="match: GSS: Em:AL274269" /note="AluSx repeat: matches 1..300 of consensus"
misc-feature	51395..51549	/note="match: GSS: Em:AZ050850"
misc-feature	complement(52049..52621)	/gene="bA408E5.3"
misc-feature	complement(52206..52621)	/note="match: GSS: Em:AQ385258" /gene="bA408E5.3"
misc-feature	complement(52293..52630)	/note="match: GSS: Em:AQ385348" /gene="bA408E5.3"
repeat-region	53154..53428	/note="match: GSS: Em:AQ730403"
repeat-region	53553..53656	/note="LTR33 repeat: matches 12..295 of consensus"
repeat-region	53657..53942	/note="AluJb repeat: matches 1..100 of consensus"
repeat-region	53943..54126	/note="AluY repeat: matches 1..292 of consensus"
repeat-region	53943..54126	/note="AluJb repeat: matches 100..299 of consensus"
repeat-region	54205..54457	/note="AluJo repeat: matches 41..296 of consensus"
repeat-region	55545..55826	/note="AluSx repeat: matches 12..311 of consensus"
repeat-region	55828..55862	/note="LTR23 repeat: matches 385..419 of consensus"
repeat-region	55863..56188	/note="AluSx repeat: matches 1..308 of consensus"
repeat-region	56189..56328	/note="LTR23 repeat: matches 245..385 of consensus"
repeat-region	56335..56407	/note="FLAM repeat: matches 46..118 of consensus"
repeat-region	56420..56651	/note="LTR23 repeat: matches 2..252 of consensus"
repeat-region	56796..56911	/note="FLAM-A repeat: matches 17..130 of consensus"

repeat-region	57328..57668	/note="MLT1A2 repeat: matches 2..372 of consensus"
repeat-region	57746..58041	/note="Tigger3(Golem) repeat: matches 1..3028 of consensus"
mRNA	join(58370..58490, 60268..60512, 60609..60652)	/gene="bA408E5.4"
		/note="match: cDNAs: Em:AF128625 Em:AB032950 Em:AF021936 match: ESTs: Em:AW177973 Em:AI832126" /product="bA408E5.4 (novel protein similar to DMPK-like CDC42-binding protein kinase beta (CDC42BPB))" /evidence=not-experimental /gene="bA408E5.4"
gene	58370..60652	
CDS	join(58458..58490, 60268..60474)	/gene="bA408E5.4"
		/note="match: proteins: Tr:Q9ULU5 Tr:O54875 Tr:Q9Y5S2 Tr:O54874" /codon-start=1 /evidence=not-experimental /product="bA408E5.4 (novel protein similar to DMPK-like CDC42-binding protein kinase beta (CDC42BPB))" /protein-id="CAC12715.1" /db-xref="GI:10697002" /translation="MVWQENEDLRKQLVEASELL KSQAKELKDAHQQQKLALQDFLEL CELVAELCSQKQKVWDKEGEMEAMQKVNTMWQES"
repeat-region	59470..59661	/note="12 copies 16 mer 66% conserved"
repeat-region	59671..59700	/note="BC200 repeat: matches 134..162 of consensus"
repeat-region	59701..59825	/note="AluJb repeat: matches 3..125 of consensus"
misc-feature	complement(59740..60244)	/note="match: GSS: Em:B14221"
repeat-region	59846..59909	/note="4 copies 16 mer 79% conserved"
misc-feature	complement(60460..61074)	/note="match: GSS: Em:AQ739924"
repeat-region	60608..60909	/note="AluY repeat: matches 1..300 of consensus"
misc-feature	complement(60900..61074)	/note="match: GSS: Em:AQ828361"
misc-feature	complement(60929..61074)	/note="match: GSS: Em:AQ199477"
repeat-region	61077..61383	/note="AluY repeat: matches 1..304 of consensus"
repeat-region	61384..61468	/note="MSTA-internal repeat: matches 1502..1580 of consensus"
repeat-region	61469..61839	/note="MSTA repeat: matches 1..426 of consensus"
repeat-region	62988..63051	/note="4 copies 16 mer 78% conserved"
repeat-region	63191..63251	/note="L2 repeat: matches 2641..2701 of consensus"
repeat-region	63250..63297	/note="3 copies 16 mer 87% conserved"
repeat-region	63673..64099	/note="L1MEc repeat: matches 927..1323 of consensus"
repeat-region	64100..64397	/note="AluSx repeat: matches 1..294 of consensus"

repeat-region	64398..64418	/note="L1MEc repeat: matches 1323..1341 of consensus"
repeat-region	64419..64712	/note="AluSc repeat: matches 1..294 of consensus"
repeat-region	64713..64826	/note="L1MEc repeat: matches 1341..1529 of consensus"
repeat-region	64885..65144	/note="AluSg repeat: matches 35..294 of consensus"
repeat-region	65146..65193	/note="3 copies 16 mer 95% conserved"
repeat-region	65192..65472	/note="L1MEc repeat: matches 1541..1822 of consensus"
repeat-region	65473..65770	/note="AluSg repeat: matches 1..299 of consensus"
repeat-region	65771..65865	/note="L1MEc repeat: matches 1822..1916 of consensus"
repeat-region	65866..66155	/note="AluJb repeat: matches 1..292 of consensus"
repeat-region	66513..66681	/note="L1 repeat: matches 3455..3622 of consensus"
repeat-region	66682..66975	/note="AluSx repeat: matches 1..301 of consensus"
repeat-region	66976..67020	/note="L1 repeat: matches 3622..3666 of consensus"
repeat-region	67024..67144	/note="L1M4 repeat: matches 5686..5813 of consensus"
repeat-region	67150..67335	/note="AluSc repeat: matches 137..309 of consensus"
repeat-region	67336..67612	/note="AluSg repeat: matches 1..301 of consensus"
repeat-region	67613..67745	/note="AluSc repeat: matches 1..137 of consensus"
repeat-region	67751..68262	/note="L1M4 repeat: matches 5005..5488 of consensus"
repeat-region	68263..68576	/note="AluSq repeat: matches 1..310 of consensus"
repeat-region	68577..68607	/note="L1M4 repeat: matches 4977..5005 of consensus"
repeat-region	68608..68898	/note="AluSx repeat: matches 1..296 of consensus"
repeat-region	68899..68910	/note="L1M4 repeat: matches 4967..4977 of consensus"
repeat-region	68911..69214	/note="AluSx repeat: matches 1..301 of consensus"
repeat-region	69215..69345	/note="L1M4 repeat: matches 4844..4967 of consensus"
repeat-region	69346..69669	/note="AluJb repeat: matches 1..308 of consensus"
repeat-region	69670..69905	/note="L1M4 repeat: matches 4571..4844 of consensus"
repeat-region	69906..70177	/note="AluJb repeat: matches 1..285 of consensus"
repeat-region	70267..70924	/note="L1M4 repeat: matches 3169..3871 of consensus"
repeat-region	71018..71344	/note="AluSx repeat: matches 1..311 of consensus"
repeat-region	71357..71538	/note="AluSq repeat: matches 121..307 of consensus"
repeat-region	71649..71955	/note="AluSx repeat: matches 6..312 of consensus"
repeat-region	72237..72425	/note="MLT1B repeat: matches 1..187 of consensus"
repeat-region	73729..73762	/note="17 copies 2 mer aa 91% conserved"

misc-feature	74514..74918	/note="match: STS: Em:G38482"
repeat-region	75337..75511	/note="AluY repeat: matches 124..293 of consensus"
repeat-region	77025..77333	/note="AluSg repeat: matches 1..309 of consensus"
misc-feature	join(77917..77950, 78264..78786)	/note="match: GSS: Em:AQ111592"
repeat-region	77957..78260	/note="AluY repeat: matches 1..302 of consensus"
misc-feature	80700..81062	/note="match: GSS: Em:B36622"
misc-feature	80700..81056	/note="match: GSS: Em:B36630"
misc-feature	80706..81067	/note="match: GSS: Em:AQ197250"
misc-feature	complement(80784..81400)	/note="match: GSS: Em:B90473"
repeat-region	80983..81268	/note="AluJb repeat: matches 11..300 of consensus"
misc-feature	81401..81903	/note="match: GSS: Em:AQ036965"
misc-feature	81434..81876	/note="match: GSS: Em:AQ676662"
misc-feature	complement(82301..82561)	/note="match: GSS: Em:AQ014105"
repeat-region	82935..83210	/note="AluJo repeat: matches 17..290 of consensus"
repeat-region	83211..83451	/note="AluSg/x repeat: matches 71..310 of consensus"
repeat-region	83461..83611	/note="FRAM repeat: matches 1..152 of consensus"
repeat-region	83983..84856	/note="L1MC1 repeat: matches 5415..6316 of consensus"
repeat-region	84926..85040	/note="FLAM-A repeat: matches 1..117 of consensus"
misc-feature	complement(85113..85449)	/note="match: GSS: Em:AQ166233"
repeat-region	85451..85750	/note="AluY repeat: matches 1..299 of consensus"
repeat-region	85756..85869	/note="FLAM-A repeat: matches 5..116 of consensus"
misc-feature	complement(85916..86247)	/note="match: GSS: Em:B95847"
repeat-region	85973..90021	/note="L1P repeat: matches 5..4052 of consensus"
repeat-region	90029..92862	/note="L1P repeat: matches 1..2835 of consensus"
repeat-region	93130..93416	/note="AluSx repeat: matches 1..287 of consensus"
misc-feature	93219..93416	/note="match: GSS: Em:AQ752888"
misc-feature	complement(93250..93416)	/note="match: STS: Em:AF191981"
misc-feature	93269..93416	/note="match: GSS: Em:AQ411530"
misc-feature	complement(93271..93416)	/note="match: GSS: Em:B37823"
repeat-region	93462..93518	/note="AluS repeat: matches 1..57 of consensus"
repeat-region	93655..93777	/note="AluJb repeat: matches 13..140 of consensus"
misc-feature	complement(93680..93845)	/note="match: GSS: Em:AQ388066"
repeat-region	93778..94079	/note="AluSp repeat: matches 1..302 of consensus"
repeat-region	94096..94240	/note="AluJo/FRAM repeat: matches 156..299 of consensus"
misc-feature	94442..94770	/note="match: GSS: Em:AQ601852"
repeat-region	94704..94962	/note="AluSx repeat: matches 25..285 of consensus"
repeat-region	95267..95491	/note="AluY repeat: matches

repeat-region	95645..95779	70..294 of consensus" /note="AluSc repeat: matches 169..306 of consensus"
repeat-region	95780..96109	/note="AluSg repeat: matches 12..304 of consensus"
repeat-region	96119..96389	/note="AluSx repeat: matches 1..295 of consensus"
repeat-region	96506..96799	/note="AluSx repeat: matches 1..296 of consensus"
repeat-region	97009..97301	/note="AluJo repeat: matches 1..292 of consensus"
repeat-region	97439..97531	/note="AluSg/x repeat: matches 204..300 of consensus"
repeat-region	98100..98198	/note="MER5A repeat: matches 94..189 of consensus"
repeat-region	98224..98356	/note="AluSx repeat: matches 1..133 of consensus"
repeat-region	98361..98653	/note="AluSx repeat: matches 1..293 of consensus"
repeat-region	98743..98914	/note="AluSg/x repeat: matches 131..302 of consensus"
misc-feature	98989..99230	/note="match: GSS: Em:AQ200713"
misc-feature	99087..99259	/note="match: GSS: Em:B78965 Em:B88275"
repeat-region	99385..99552	/note="AluSx repeat: matches 123..288 of consensus"
repeat-region	99553..99616	/note="4 copies 16 mer 78% conserved"
repeat-region	99562..99611	/note="25 copies 2 mer at 76% conserved"
repeat-region	99904..100195	/note="AluSp repeat: matches 2..295 of consensus"
repeat-region	101022..101163	/note="L2 repeat: matches 2601..2750 of consensus"
repeat-region	101279..101366	/note="AluJ/FLAM repeat: matches 3..90 of consensus"
repeat-region	101423..101492	/note="AluJb repeat: matches 219..288 of consensus"
repeat-region	101493..101799	/note="AluSq repeat: matches 1..309 of consensus"
repeat-region	101800..102020	/note="AluJb repeat: matches 1..219 of consensus"
repeat-region	102584..102899	/note="AluSq repeat: matches 1..312 of consensus"
repeat-region	102988..103258	/note="AluSx repeat: matches 1..282 of consensus"
repeat-region	103470..103762	/note="AluJb repeat: matches 1..300 of consensus"
repeat-region	103807..104081	/note="AluSq repeat: matches 1..296 of consensus"
repeat-region	104118..104281	/note="L2 repeat: matches 1430..1594 of consensus"
repeat-region	104435..104549	/note="AluSq/x repeat: matches 3..117 of consensus"
repeat-region	104552..104919	/note="L1PA15 repeat: matches 2718..3080 of consensus"
repeat-region	104920..105215	/note="AluSp repeat: matches 16..312 of consensus"
repeat-region	105216..108284	/note="L1PA15 repeat: matches 3080..6157 of consensus"
repeat-region	109704..110006	/note="AluSx repeat: matches 1..302 of consensus"
repeat-region	110500..110551	/note="L1M2 repeat: matches 85..137 of consensus"

repeat-region	110552..111337	/note="L1MA3 repeat: matches 5501..6303 of consensus"
repeat-region	111696..112155	/note="L1 repeat: matches 2795..3298 of consensus"
repeat-region	112221..112290	/note="L1M3c repeat: matches 927..995 of consensus"
repeat-region	112478..112708	/note="L1M3c repeat: matches 157..617 of consensus"
repeat-region	112735..112931	/note="MLT1F repeat: matches 197..456 of consensus"
misc-feature	complement(114438..114920)	/note="match: GSS: Em:AQ463381"
misc-feature	complement(114447..114907)	/note="match: GSS: Em:AQ768845"
repeat-region	114799..116584	/note="L1PBa repeat: matches -1545..1234 of consensus"
repeat-region	116596..117661	/note="L1PBa repeat: matches -1545..-412 of consensus"
repeat-region	117649..118842	/note="L1PBa repeat: matches -279..1792 of consensus"
misc-feature	complement(118561..11917)	/note="match: GSS: Em:AQ631395"
misc-feature	complement(118565..11917)	/note="match: GSS: Em:AQ417340"
misc-feature	complement(118657..11917)	/note="match: GSS: Em:AQ374370"
misc-feature	complement(118667..11917)	/note="match: GSS: Em:AQ751324 Em:AQ751359"
misc-feature	complement(118721..11917)	/note="match: GSS: Em:B84833"
misc-feature	118755..119117	/note="match: STS: Em:HS537P22S"
misc-feature	complement(118792..11917)	/note="match: GSS: Em:AQ266754"
misc-feature	118947..119117	/note="match: GSS: Em:AQ478093"
misc-feature	complement(118948..11917)	/note="match: GSS: Em:AQ129513 Em:AQ252185"
misc-feature	118948..119117	/note="match: GSS: Em:B35471"
misc-feature	complement(118950..11917)	/note="match: GSS: Em:AQ342726"
misc-feature	118961..119117	/note="match: GSS: Em:AQ771365"
misc-feature	118965..119117	/note="match: GSS: Em:AQ239606"
misc-feature	119015..119117	/note="match: GSS: Em:AQ589275"
misc-feature	119017..119107	/note="match: GSS: Em:AQ550747"
misc-feature	join(119020..119125, 119450..119508)	/note="match: GSS: Em:AQ708727"
misc-feature	119025..119117	/note="match: GSS: Em:AQ488170"
misc-feature	119025..119113	/note="match: GSS: Em:AQ679687"
repeat-region	119050..119061	/note="L1 repeat: matches 1888..2002 of consensus"
misc-feature	join(119056..119135, 119441..119534)	/note="match: GSS: Em:AQ280833"
misc-feature	join(119115..119120, 119438..119579)	/note="match: GSS: Em:AQ679687"
misc-feature	complement(119146..119549)	/note="match: GSS: Em:AQ239248"
misc-feature	complement(119211..119595)	/note="match: GSS: Em:AQ720265"
misc-feature	119442..119637	/note="match: GSS: Em:AQ550747"
repeat-region	119458..121708	/note="L1M1 repeat: matches 2446..4326 of consensus"
repeat-region	121711..121791	/note="L1 repeat: matches 4213..4293 of consensus"
repeat-region	122563..124403	/note="L1PB1 repeat: matches 4278..6155 of consensus"

repeat-region	124416..124801	/note="L1PBa repeat: matches 1220..1606 of consensus"
misc-feature	124776..124988	/note="match: GSS: Em:AQ426784"
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misc-feature	complement(124796..124973)	/note="match: GSS: Em:B71736"
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misc-feature	complement(124806..124980)	/note="match: GSS: Em:AQ767686"
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misc-feature	complement(124806..124975)	/note="match: GSS: Em:AQ744794"
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misc-feature	124849..125252	/note="match: GSS: Em:AQ740214"
misc-feature	124893..125075	/note="match: GSS: Em:AQ432854"
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misc-feature	124894..125158	/note="match: GSS: Em:AQ609735"
misc-feature	124894..125142	/note="match: GSS: Em:AQ201407"
misc-feature	124894..125121	/note="match: GSS: Em:B99068"
repeat-region	124894..128908	/note="L1PB1 repeat: matches 2121..6154 of consensus"
misc-feature	124982..125207	/note="match: GSS: Em:AQ486704"
misc-feature	124990..125224	/note="match: GSS: Em:AQ771768"
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misc-feature	124992..125159	/note="match: GSS: Em:AQ426784 Em:AQ734454"
repeat-region	129486..129619	/note="L1M repeat: matches 5258..5395 of consensus"
misc-feature	130452..130804	/note="match: GSS: Em:AQ809949"
misc-feature	130463..131161	/note="match: GSS: Em:AQ551018"
misc-feature	130507..130804	/note="match: GSS: Em:AQ135436"
misc-feature	130807..130966	/note="match: GSS: Em:AQ809949"
repeat-region	132779..132990	/note="TIGGER2 repeat: matches 336..548 of consensus"
repeat-region	133042..133184	/note="L1MA3 repeat: matches 6149..6288 of consensus"
repeat-region	133185..133487	/note="AluSp repeat: matches 14..309 of consensus"
misc-feature	133190..133486	/note="match: GSS: Em:AQ752084"
misc-feature	complement(133201..133487)	/note="match: GSS: Em:AQ529189"
misc-feature	complement(133270..133435)	/note="match: GSS: Em:AQ016362"
repeat-region	133538..134403	/note="L1MC4 repeat: matches 7134..7971 of consensus"
repeat-region	134507..135118	/note="L1MC4 repeat: matches 7167..7829 of consensus"
repeat-region	135186..135221	/note="18 copies 2 mer aa 80%

repeat-region	135542..135845	conserved"
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		/note="match: cDNAs: Em:AB028997 Em:AF172850 Em:AB021644 Em:AL137351 match: ESTs: Em:AA994611 Em:AI215068" /product="bA408E5.5.2 (novel protein isoform 2)" /evidence=not-experimental
polyA-site	complement(135945)	/gene="bA408E5.5"
mRNA	complement(join(135945..136179,136358..136431,136931..137021))	/gene="bA408E5.5"
		/note="match: cDNAs: Em:AF172850 Em:AB021644 Em:AB028997 Em:AL137351 match: ESTs: Em:AI215068 Em:AA994611" /product="bA408E5.5.1 (novel protein isoform 1)" /evidence=not-experimental
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polyA-site	complement(135948)	/gene="bA408E5.5"
polyA-signal	complement(135964..135969)	/gene="bA408E5.5"
repeat-region	136400..136898	/note="L2 repeat: matches 2186..2710 of consensus"
misc-feature	137333..137635	/note="match: GSS: Em:AQ061528"
repeat-region	137705..138496	/note="MER4D repeat: matches 237..973 of consensus"
misc-feature	complement(138179..138535)	/note="match: GSS: Em:AQ549616"
misc-feature	complement(138216..138535)	/note="match: GSS: Em:AQ697599"
misc-feature	complement(138253..138533)	/note="match: STS: Em:G41989"
misc-feature	complement(138296..138533)	/note="match: GSS: Em:AQ777735"
misc-feature	complement(138321..138571)	/note="match: GSS: Em:AQ024506"
misc-feature	complement(138338..138533)	/note="match: GSS: Em:AQ207684"
misc-feature	complement(138357..138560)	/note="match: GSS: Em:AQ815465"
misc-feature	complement(138374..138527)	/note="match: GSS: Em:AQ550470"
misc-feature	complement(138395..138535)	/note="match: GSS: Em:AQ037473"
repeat-region	140212..140301	/note="MIR repeat: matches 59..146 of consensus"
misc-feature	141017..141343	/note="match: GSS: Em:AQ442921"
repeat-region	142426..142509	/note="L2 repeat: matches 2612..2695 of consensus"
repeat-region	142949..144874	/note="L1P3 repeat: matches 299..1824 of consensus"
repeat-region	144875..145159	/note="L1PA6 repeat: matches 5865..6141 of consensus"
repeat-region	145160..146143	/note="L1P3 repeat: matches 1824..2842 of consensus"
repeat-region	146144..146916	/note="L1P repeat: matches 3..776 of consensus"

repeat-region 146912..149559

/note="L1P repeat: matches
900..3549 of consensus"

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LOCUS (LOC): **AL162272** GenBank (R)
 GenBank ACC. NO. (GBN): **AL162272**
 GenBank VERSION (VER): AL162272.10 GI:10045365
 CAS REGISTRY NO. (RN): 260338-28-1
 SEQUENCE LENGTH (SQL): 154904
 MOLECULE TYPE (CI): DNA; linear
 DIVISION CODE (CI): Primates
 DATE (DATE): 22 Dec 2000
 DEFINITION (DEF): Human DNA sequence from clone RP11-145E8 on chromosome 10. Contains the gene KIAA1074, the 3' end of the YME1L1 gene for YME1 (S.cerevisiae)-like 1, ESTs, STSS, GSSs and a CpG island, complete sequence.
 KEYWORDS (ST): HTG; CpG island; KIAA1074; YME1L1
 SOURCE: Homo sapiens (human)
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 49646 a 30704 c 29517 g 45037 t
 COMMENT:

On Sep 9, 2000 this sequence version replaced gi:9864502.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10>
 This sequence is the entire insert of clone RP11-145E8 The true left end of clone RP11-85G18 is at 127454 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-145E8 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACe3.6.

REFERENCE: 1 (bases 1 to 154904)
 AUTHOR (AU): Bird,C.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (11-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..154904	/organism="Homo sapiens" /mol-type="genomic DNA" /db-xref="taxon:9606" /chromosome="10" /clone="RP11-145E8"

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		/note="L1M4c repeat: matches 1639..1853 of consensus"
misc-feature	15..494	/note="match: GSS: Em:AQ373109"
repeat-region	431..732	/note="AluJo repeat: matches 1..304 of consensus"
repeat-region	766..1074	/note="AluSx repeat: matches 1..309 of consensus"
repeat-region	1358..1420	/note="LTR40b repeat: matches 1..54 of consensus"
repeat-region	1421..1720	/note="AluSx repeat: matches 1..300 of consensus"
repeat-region	1721..1805	/note="LTR40b repeat: matches 54..169 of consensus"
repeat-region	1886..1943	/note="LTR40a repeat: matches 240..297 of consensus"
repeat-region	1942..2144	/note="LTR40a repeat: matches 209..409 of consensus"
repeat-region	3375..3688	/note="AluSx repeat: matches 1..309 of consensus"
repeat-region	4147..4449	/note="AluSg1 repeat: matches 1..304 of consensus"
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misc-feature	complement(6406..6941)	/note="match: GSS: Em:AQ483279"
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repeat-region	7242..7615	/note="MER4A repeat: matches 1..349 of consensus"
repeat-region	7625..7848	/note="MER4-internal repeat: matches 6385..6595 of consensus"
repeat-region	8245..8372	/note="HERVL18 repeat: matches 5621..5748 of consensus"
misc-feature	complement(8517..8948)	/note="match: GSS: Em:AQ701117"
repeat-region	11060..12633	/note="L1PA2 repeat: matches 4566..6139 of consensus"
repeat-region	13718..13863	/note="HERV17 repeat: matches 4073..4221 of consensus"
repeat-region	13971..14101	/note="FLAM-C repeat: matches 2..132 of consensus"
repeat-region	15953..16136	/note="MER4-internal repeat: matches 473..673 of consensus"
repeat-region	16204..16479	/note="MER4-internal repeat: matches 1..283 of consensus"
repeat-region	16568..16624	/note="MER4C repeat: matches 300..356 of consensus"
repeat-region	16646..16934	/note="AluSp repeat: matches 13..297 of consensus"
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repeat-region	17121..17461	/note="MER4A repeat: matches 1..323 of consensus"
repeat-region	17664..17733	/note="35 copies 2 mer ac 82% conserved"
repeat-region	18057..18237	/note="HERVL18 repeat: matches 5621..5801 of consensus"
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misc-feature	18845..19280	/note="match: GSS: Em:AQ270943"
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repeat-region	22813..22904	1..287 of consensus"
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repeat-region	25573..25901	427..568 of consensus"
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repeat-region	25928..26239	4077..4445 of consensus"
		/note="AluYb8 repeat: matches
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repeat-region	53358..53520	/note="MER46B repeat: matches 23..190 of consensus"
repeat-region	53521..53812	/note="AluY repeat: matches 1..302 of consensus"
repeat-region	53813..53999	/note="MER46B repeat: matches

repeat-region	54615..54797	190..236 of consensus" /note="MER58A repeat: matches 38..220 of consensus"
repeat-region	55074..55279	/note="MIR repeat: matches 35..238 of consensus"
repeat-region	56418..56922	/note="L1MB8 repeat: matches 5651..6167 of consensus"
misc-feature	56614..57363	/note="match: GSS: Em:AQ547539"
misc-feature	56617..57229	/note="match: GSS: Em:AQ542726"
repeat-region	57427..57558	/note="AluSx repeat: matches 5..137 of consensus"
repeat-region	57559..57871	/note="AluSx repeat: matches 1..312 of consensus"
repeat-region	57872..58045	/note="AluSx repeat: matches 137..307 of consensus"
repeat-region	58075..58312	/note="AluY repeat: matches 80..305 of consensus"
misc-feature	complement(58300..58752)	/gene="bA145E8.1" /note="match: GSS: Em:AQ561539"
misc-feature	complement(58300..58637)	/gene="bA145E8.1"
misc-feature	complement(58300..58552)	/note="match: GSS: Em:AQ883023" /gene="bA145E8.1"
misc-feature	complement(58300..58476)	/note="match: GSS: Em:AQ424533" /gene="bA145E8.1"
misc-feature	complement(58302..58565)	/note="match: GSS: Em:AQ060557" /gene="bA145E8.1"
misc-feature	complement(58337..58643)	/note="match: GSS: Em:AQ565928" /gene="bA145E8.1"
misc-feature	complement(58357..58755)	/note="match: GSS: Em:AQ548028" /gene="bA145E8.1"
misc-feature	complement(58368..58753)	/note="match: GSS: Em:AQ539621" /gene="bA145E8.1"
misc-feature	complement(58415..58643)	/note="match: GSS: Em:AQ238461" /gene="bA145E8.1"
repeat-region	58979..59157	/note="match: GSS: Em:AQ319902"
repeat-region	61457..61534	/note="L2 repeat: matches 2154..2346 of consensus"
repeat-region	62309..62362	/note="MIR repeat: matches 176..251 of consensus"
repeat-region	62533..62931	/note="27 copies 2 mer at 70% conserved"
misc-feature	62533..62931	/note="match: GSS: Em:AQ103213"
repeat-region	62875..62921	/note="L2 repeat: matches 2664..2710 of consensus"
repeat-region	63573..63871	/note="AluSx repeat: matches 1..297 of consensus"
misc-feature	complement(64111..64364)	/gene="bA145E8.1" /note="match: GSS: Em:AQ636584 Em:AQ800192 Em:AQ811076 Em:AQ813421"
repeat-region	64378..64675	/note="AluSg repeat: matches 1..296 of consensus"
repeat-region	65454..65805	/note="L2 repeat: matches 2368..2710 of consensus"

repeat-region	65821..65953	/note="L1MEc repeat: matches 302..434 of consensus"
repeat-region	65954..66266	/note="AluSx repeat: matches 1..312 of consensus"
repeat-region	66267..66783	/note="L1MEc repeat: matches 434..982 of consensus"
repeat-region	66794..67069	/note="L1M4 repeat: matches 1237..1625 of consensus"
repeat-region	67141..67277	/note="L1MEc repeat: matches 2222..2359 of consensus"
repeat-region	67312..67540	/note="L1M4 repeat: matches 4796..4927 of consensus"
repeat-region	67541..67677	/note="AluSx repeat: matches 1..147 of consensus"
repeat-region	67678..67988	/note="AluY repeat: matches 1..311 of consensus"
repeat-region	67989..68175	/note="AluSx repeat: matches 147..299 of consensus"
repeat-region	68176..68495	/note="L1M4 repeat: matches 4927..5282 of consensus"
repeat-region	68497..68525	/note="U4 repeat: matches 1..29 of consensus"
repeat-region	68995..69299	/note="AluJo repeat: matches 1..303 of consensus"
misc-feature	69076..69577	/note="match: GSS: Em:AQ247101"
misc-feature	complement(69303..70056)	/gene="bA145E8.1"
		/note="match: GSS: Em:AQ742681"
misc-feature	complement(69350..70053)	/gene="bA145E8.1"
		/note="match: GSS: Em:AQ313554"
misc-feature	complement(69372..70030)	/gene="bA145E8.1"
		/note="match: GSS: Em:AQ312537"
repeat-region	69854..70072	/note="MIR repeat: matches 32..248 of consensus"
repeat-region	70348..70648	/note="AluSx repeat: matches 1..301 of consensus"
misc-feature	complement(70887..71030)	/gene="bA145E8.1"
		/note="match: GSS: Em:AQ035333"
repeat-region	71184..71367	/note="L2 repeat: matches 1069..1254 of consensus"
misc-feature	complement(71328..71570)	/gene="bA145E8.1"
		/note="match: GSS: Em:AQ422789"
repeat-region	71424..71528	/note="L2 repeat: matches 1380..1493 of consensus"
repeat-region	71759..71836	/note="39 copies 2 mer aa 66% conserved"
repeat-region	72545..72847	/note="AluSq repeat: matches 1..303 of consensus"
misc-feature	72806..72956	/note="match: GSS: Em:AL335780"
repeat-region	72968..73247	/note="AluSx repeat: matches 1..282 of consensus"
repeat-region	73659..73878	/note="L1M1 repeat: matches 5410..5642 of consensus"
misc-feature	complement(74344..74790)	/gene="bA145E8.1"
		/note="match: GSS: Em:AQ466492"
misc-feature	74793..75232	/note="match: GSS: Em:AQ525005"
misc-feature	74874..75116	/note="match: GSS: Em:AQ415462"
repeat-region	75147..75453	/note="AluSg repeat: matches 1..308 of consensus"

misc-feature	75574..75749	/note="match: GSS: Em:AQ262763"
misc-feature	75574..75687	/note="match: GSS: Em:AQ285147"
misc-feature	75760..76354	/note="match: GSS: Em:AQ111164"
misc-feature	complement(77188..77507)	/gene="bA145E8.1"
)	
		/note="match: GSS: Em:AQ746541"
misc-feature	complement(78121..78706)	/gene="bA145E8.1"
)	
		/note="match: GSS: Em:B90477"
repeat-region	78709..78796	/note="AluJ/FRAM repeat: matches 217..301 of consensus"
misc-feature	78879..79026	/note="match: GSS: Em:AQ745603"
misc-feature	79052..79693	/note="match: GSS: Em:AQ745603"
repeat-region	79441..79487	/note="L2 repeat: matches 2659..2705 of consensus"
repeat-region	79511..79792	/note="AluSx repeat: matches 3..298 of consensus"
repeat-region	79806..80263	/note="L2 repeat: matches 2020..2492 of consensus"
repeat-region	81148..81234	/note="L2 repeat: matches 1613..1700 of consensus"
repeat-region	81379..81671	/note="AluSx repeat: matches 13..305 of consensus"
repeat-region	81704..82006	/note="AluSp repeat: matches 1..306 of consensus"
repeat-region	82692..82715	/note="12 copies 2 mer tg 95% conserved"
repeat-region	82863..83171	/note="AluSc repeat: matches 1..309 of consensus"
repeat-region	83447..83619	/note="Charliel repeat: matches 3..199 of consensus"
repeat-region	83673..83728	/note="Charliel repeat: matches 2630..2685 of consensus"
repeat-region	83789..84081	/note="AluSc repeat: matches 1..292 of consensus"
repeat-region	84110..84419	/note="AluY repeat: matches 1..310 of consensus"
repeat-region	84471..84628	/note="L1ME1 repeat: matches 5781..5946 of consensus"
repeat-region	84734..84789	/note="Charliel repeat: matches 2706..2761 of consensus"
repeat-region	84837..85123	/note="AluSx repeat: matches 3..305 of consensus"
repeat-region	85124..85421	/note="AluSx repeat: matches 1..293 of consensus"
repeat-region	86766..87057	/note="AluJb repeat: matches 11..300 of consensus"
repeat-region	87594..87731	/note="MER5A repeat: matches 9..149 of consensus"
repeat-region	87965..88263	/note="AluSg repeat: matches 1..307 of consensus"
repeat-region	88514..88825	/note="AluSx repeat: matches 1..311 of consensus"
repeat-region	89641..89682	/note="MER57B repeat: matches 295..337 of consensus"
repeat-region	90239..90558	/note="L2 repeat: matches 2384..2732 of consensus"
misc-feature	complement(90775..90929)	/gene="bA145E8.1"
)	
		/note="match: GSS: Em:B59027"
repeat-region	90932..90959	/note="14 copies 2 mer aa 92% conserved"
repeat-region	91062..91366	/note="AluYa8 repeat: matches 1..309 of consensus"

misc-feature	91473..91785	/note="match: STS: Em:G20905"
misc-feature	complement(join(91723..92002,92330..92432))	/gene="bA145E8.1"
repeat-region	92017..92301	/note="match: GSS: Em:AG010822"
repeat-region	92566..92605	/note="AluSx repeat: matches 12..297 of consensus"
repeat-region	92639..93029	/note="MSTA repeat: matches 387..426 of consensus"
misc-feature	92749..93293	/note="match: GSS: Em:AQ039605"
misc-feature	complement(92977..93421)	/gene="bA145E8.1"
repeat-region	93040..93306	/note="match: GSS: Em:AQ715166"
misc-feature	complement(93095..93443)	/note="L2 repeat: matches 2420..2699 of consensus"
repeat-region	93307..93672	/gene="bA145E8.1"
repeat-region	93673..94123	/note="match: GSS: Em:AQ482541"
repeat-region	94124..94428	/note="THE1C repeat: matches 1..371 of consensus"
repeat-region	94429..94687	/note="L2 repeat: matches 1947..2420 of consensus"
repeat-region	94688..94814	/note="AluSg repeat: matches 7..308 of consensus"
repeat-region	94815..94860	/note="L2 repeat: matches 1759..1947 of consensus"
repeat-region	95046..95328	/note="FLAM-C repeat: matches 1..127 of consensus"
repeat-region	95329..95625	/note="L2 repeat: matches 1712..1759 of consensus"
repeat-region	95876..96170	/note="AluJo repeat: matches 5..304 of consensus"
repeat-region	96366..96679	/note="AluSx repeat: matches 1..302 of consensus"
repeat-region	96743..99604	/note="AluSg repeat: matches 1..294 of consensus"
repeat-region	99605..99899	/note="AluY repeat: matches 1..305 of consensus"
repeat-region	99900..100019	/note="L1PBb repeat: matches -1540..1345 of consensus"
repeat-region	100053..101455	/note="AluSx repeat: matches 1..296 of consensus"
repeat-region	101456..101768	/note="L1PBb repeat: matches 1345..1458 of consensus"
repeat-region	101769..102478	/note="L1P repeat: matches 1750..3220 of consensus"
misc-feature	complement(103849..104402)	/note="AluSq repeat: matches 3..313 of consensus"
misc-feature	complement(104053..104402)	/note="L1P repeat: matches 3220..3912 of consensus"
misc-feature	104403..104689	/gene="bA145E8.1"
misc-feature	104417..104819	/note="match: GSS: Em:AQ420316"
misc-feature	104439..104774	/gene="bA145E8.1"
repeat-region	104781..105079	/note="match: GSS: Em:AQ420311"
repeat-region	105082..105390	/note="match: GSS: Em:AQ460970"
		/note="match: GSS: Em:AQ202037"
		/note="match: GSS: Em:AQ570839"
		/note="AluSx repeat: matches 4..303 of consensus"
		/note="AluYb8 repeat: matches 1..316 of consensus"

repeat-region	106904..106950	/note="L1PA14 repeat: matches 5761..5746 of consensus"
repeat-region	106951..107241	/note="AluY repeat: matches 1..292 of consensus"
repeat-region	107242..107334	/note="L1PA14 repeat: matches 5745..5862 of consensus"
repeat-region	107256..107299	/note="22 copies 2 mer aa 81% conserved"
repeat-region	107745..107908	/note="MIR repeat: matches 16..190 of consensus"
repeat-region	108216..108386	/note="L2 repeat: matches 1804..1969 of consensus"
repeat-region	108566..108645	/note="40 copies 2 mer aa 65% conserved"
repeat-region	108648..108781	/note="FLAM-C repeat: matches 1..133 of consensus"
repeat-region	108971..109119	/note="MER58A repeat: matches 2..151 of consensus"
repeat-region	109139..109452	/note="AluJb repeat: matches 1..310 of consensus"
repeat-region	109792..110096	/note="AluSq repeat: matches 1..301 of consensus"
repeat-region	110302..110604	/note="AluSg repeat: matches 1..303 of consensus"
misc-feature	complement(110605..110724)	/gene="bA145E8.1"
repeat-region	110912..111339	/note="match: GSS: Em:AQ227361"
repeat-region	111968..112277	/note="Tigger2a repeat: matches 5..434 of consensus"
repeat-region	111968..112277	/note="AluSg repeat: matches 1..308 of consensus"
misc-feature	112285..112428	/note="match: GSS: Em:B44336"
repeat-region	112411..112559	/note="MIR repeat: matches 57..215 of consensus"
misc-feature	112432..112629	/note="match: GSS: Em:B44336"
repeat-region	112999..113291	/note="AluJo repeat: matches 1..291 of consensus"
repeat-region	113528..113633	/note="U6 repeat: matches 1..106 of consensus"
repeat-region	114716..115020	/note="AluJo repeat: matches 1..306 of consensus"
repeat-region	115370..115623	/note="AluSx repeat: matches 1..307 of consensus"
misc-feature	115941..116435	/note="match: GSS: Em:AQ238956"
misc-feature	115958..116532	/note="match: GSS: Em:B85821"
repeat-region	116020..116302	/note="AluSp repeat: matches 1..286 of consensus"
repeat-region	116373..116571	/note="MIR repeat: matches 14..230 of consensus"
misc-feature	116527..116867	/note="match: GSS: Em:AQ030505"
repeat-region	116649..116702	/note="27 copies 2 mer aa 70% conserved"
repeat-region	116912..117204	/note="AluSg repeat: matches 1..293 of consensus"
repeat-region	118007..118306	/note="AluSx repeat: matches 1..294 of consensus"
misc-feature	118360..118885	/note="match: STS: Em:HSJ35H5"
misc-feature	118888..119045	/note="match: STS: Em:HSJ35H5"
repeat-region	119096..119494	/note="THE1C repeat: matches 1..371 of consensus"
repeat-region	119609..119835	/note="MIR repeat: matches 20..262 of consensus"
repeat-region	119926..120222	/note="AluSg repeat: matches 1..296 of consensus"

repeat-region	120592..120888	/note="AluSx repeat: matches 1..297 of consensus"
misc-feature	120683..121195	/note="match: GSS: Em:AQ734455"
repeat-region	121688..121997	/note="AluSx repeat: matches 1..308 of consensus"
repeat-region	122114..122399	/note="AluSx repeat: matches 9..294 of consensus"
repeat-region	122400..122683	/note="AluY repeat: matches 1..297 of consensus"
misc-feature	complement(122453..123078)	/gene="bA145E8.1"
repeat-region	122694..122746	/note="match: GSS: Em:AQ378994"
repeat-region	122844..123158	/note="L2 repeat: matches 2658..2710 of consensus"
repeat-region	122844..123158	/note="AluSx repeat: matches 1..312 of consensus"
repeat-region	123313..123358	/note="23 copies 2 mer tt 78% conserved"
repeat-region	123391..123516	/note="FLAM-C repeat: matches 1..126 of consensus"
repeat-region	123759..124054	/note="AluY repeat: matches 1..295 of consensus"
repeat-region	124189..124496	/note="AluSq repeat: matches 1..308 of consensus"
repeat-region	124636..124885	/note="AluJo repeat: matches 2..302 of consensus"
misc-feature	125353..125899	/note="CpG island"
repeat-region	126317..126625	/evidence=not-experimental
repeat-region	126317..126625	/note="AluJb repeat: matches 1..307 of consensus"
misc-feature	complement(126901..127346)	/note="match: GSS: Em:AQ581210"
repeat-region	126971..127242	/note="AluSx repeat: matches 29..311 of consensus"
repeat-region	127744..128045	/note="AluY repeat: matches 1..298 of consensus"
repeat-region	128538..128658	/note="FLAM-C repeat: matches 1..121 of consensus"
repeat-region	128763..128833	/note="LTR41 repeat: matches 703..771 of consensus"
repeat-region	128854..128996	/note="AluJo repeat: matches 6..163 of consensus"
repeat-region	128997..129313	/note="AluSx repeat: matches 2..305 of consensus"
repeat-region	129324..129627	/note="AluSx repeat: matches 3..304 of consensus"
repeat-region	129628..129714	/note="AluJo repeat: matches 173..220 of consensus"
repeat-region	129746..130039	/note="AluSg repeat: matches 1..295 of consensus"
repeat-region	130751..130863	/note="LTR41 repeat: matches 654..766 of consensus"
repeat-region	131040..131292	/note="AluSg repeat: matches 14..295 of consensus"
repeat-region	131965..132010	/note="23 copies 2 mer ta 87% conserved"
repeat-region	132015..132132	/note="59 copies 2 mer at 59% conserved"
repeat-region	132250..132556	/note="AluSx repeat: matches 1..306 of consensus"
repeat-region	132909..133690	/note="L1MEc repeat: matches 1094..1927 of consensus"
repeat-region	133781..134060	/note="AluSx repeat: matches 1..282 of consensus"

repeat-region	134132..134250	/note="L1MEc repeat: matches 2095..2217 of consensus"
repeat-region	134251..134564	/note="AluY repeat: matches 1..309 of consensus"
repeat-region	134575..134877	/note="AluY repeat: matches 1..302 of consensus"
repeat-region	134896..135226	/note="L1M4 repeat: matches 5254..5602 of consensus"
misc-feature	complement(135144..135609)	/note="match: GSS: Em:AQ221837"
repeat-region	135238..135362	/note="L1ME1 repeat: matches 6018..6163 of consensus"
repeat-region	135457..135565	/note="L1MC4 repeat: matches 7861..7972 of consensus"
misc-feature	135613..136042	/note="match: GSS: Em:AQ038825"
gene	complement(135660..151992)	/gene="YME1L1"
mRNA	complement(join(135660..137326,139727..139813,141266..141339,141425..141551,142782..142933,144500..144655,145641..145753,146592..146654,148047..148179,148753..148905,151902..>151992))	/gene="YME1L1"

/product="bA145E8.2 (YME1 (S.cerevisiae)-like 1)"
 /note="match: cDNAs: Em:AF090430 Em:AJ132637 Em:AK001259 Em:X81986 match: ESTs: Em:BE883539 Em:AU124650 Em:AU139800 Em:BE614349 Em:AU137694 Em:AV758758 Em:BF045780 Em:AI961692 Em:BF035253 Em:AI804495 Em:AU153522 Em:AA418590 Em:AI635319 Em:BE307502 Em:AW475743 Em:AU118050 Em:BE653388 Em:BE780429 Em:AI802380 Em:AU128765 Em:AV692709 Em:H66548 Em:BE966378 Em:AA452392 Em:W27884 Em:AW058381 Em:BE783242 Em:R24937 Em:AV611597 Em:BE222029 Em:AW189345 Em:BF103811 Em:AI927302 Em:BE633677 Em:AW571851 Em:AU151135 Em:AI435930 Em:BE686244 Em:BE635019 Em:BE644837 Em:AI984163 Em:AW465246 Em:AW138746 Em:AA448963 Em:BE368732 Em:C17550 Em:AW917594 Em:AV738729 Em:BB180843 Em:AV666087 Em:AW902730 Em:W39674 Em:AI755119 Em:AI351372 Em:F12257 Em:AW902476 Em:BB514618 Em:AW988172 Em:AW902455 Em:AW902478 Em:AW494343 Em:AA354203 Em:AW261890 Em:AW136841 Em:T65313 Em:BF114722 Em:AA707268 Em:AW902479 Em:BE939651 Em:AA827216

Em:AW902720 Em:AA851274 Em:D78825
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 Em:AW902483 Em:BE929397
 Em:AW902729 Em:AI004693
 Em:AA453670 Em:AA418574 Em:P54813
 Em:AA452161 Em:AU149020
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 Em:AW902469 Em:AI634166
 Em:AW902461 Em:AU153938
 Em:AW410234 Em:AA680213
 Em:BF085286 Em:AA215779 Em:F06869
 Em:AW235766 Em:AI232659
 Em:AU156536 Em:AA621081
 Em:AA466714 Em:AW015422 Em:F06870
 Em:AW139700 Em:AA067680
 Em:BE349597 Em:BE720589
 Em:AI631474 Em:AI910343
 Em:AA618016 Em:AA447738
 Em:AA675015 Em:AI739557
 Em:BE613637 Em:AW902737
 Em:BE779478 Em:AW902734 Em:W44815
 Em:AL121142 Em:BE588799 Em:AW3
 41254 Em:AI859728 Em:AI094228
 Em:BE780049 Em:F06886 Em:AA903638
 Em:AI427673 Em:AA993180 Em:N55752
 Em:AW075704 Em:AW953636 Em:N99489
 Em:AA580688 Em:AI904692
 Em:AW193861 Em:H41985 Em:AA732285
 Em:T03326 Em:BF094361 Em:AA455981
 Em:AW963623 Em:AW063992
 Em:AU138715 Em:D25558 Em:AI301983
 Em:AW369696 Em:AW595355
 Em:AW339656 Em:AI832869
 Em:AL047192 Em:AW198067 Em:N72036
 Em:AI618498 Em:AI267921 Em:C06118
 Em:AA075084 Em:M87933 Em:AI032259
 Em:N74936 Em:W23553 Em:AW955309
 Em:BF089756 Em:AI982808
 Em:AW770803 Em:AI638081
 Em:AA772630 Em:AA989107
 Em:AW500112 Em:AA355665
 Em:AA449690 Em:AA926753
 Em:AV731531 Em:AA074826
 Em:AA215671 Em:R52549 Em:AA112140
 Em:R45200 Em:AU148473 Em:AA516060
 Em:AW385823 Em:AV714080
 Em:AA789311 Em:AW964479 Em:C21168
 Em:BE047691 Em:AA580560
 Em:AA358989 Em:N35613 Em:AW591763
 Em:AI225210 Em:R46216 Em:F09884
 Em:BE201184 Em:AI400212
 Em:AA170776 Em:D57991 Em:T30730
 Em:BE737591 Em:AW770216
 Em:AI828383 Em:AA188898
 Em:AW595223 Em:AA425600
 Em:AI014395 Em:AW768484
 Em:AA513735 Em:AA425447
 Em:AI022577 Em:W27396 Em:AW467583
 Em:AI472737 Em:AI193855
 Em:AI867028 Em:AI581037
 Em:BE738578 Em:BF031128
 Em:AA015852"

/evidence=not-experimental
 /gene="YME1L1"

polyA-site

complement(135660)

polyA-signal	complement(135682..135687)	/gene="YME1L1"
misc-feature	135717..135951	/note="match: STS: Em:G20575"
repeat-region	136083..136242	/note="AluSx repeat: matches 140..291 of consensus"
repeat-region	136243..136562	/note="AluSx repeat: matches 1..311 of consensus"
repeat-region	136563..136694	/note="AluSx repeat: matches 6..140 of consensus"
misc-feature	136956..137327	/note="match: STS: Em:G29355"
CDS	complement(join(137183..137326,139727..139813,141266..141339,141425..141551,142782..142933,144500..144655,145641..145753,146592..146654,148047..148179,148753..148905,151902..>151992))	/gene="YME1L1"
		/note="match: proteins: Tr:Q9Y2Q2 Sw:P32795 Tr:O88967 Sw:Q9ZEA2 Tr:Q9UMR9 Tr:O80983 Tr:O59824 Sw:P46508 Sw:P54813" /codon-start=1 /evidence=not-experimental /product="bA145E8.2 (YME1 (S.cerevisiae)-like 1)" /protein-id="CAC19650.1" /db-xref="GI:11990780" /db-xref="GOA:Q9H1Q0" /db-xref="SPTREMBL:Q9H1Q0" /translation="VEEAKQELQEVVEFLKNPQK FTILGGKLPKGILLVGPPGTGKTL LARAVAGEADVPFYYASGSEFDEMFGVGASRIR NLFREAKANAPCVIFIDELDSVGG KRIESPMHPYSRQTINQLLAEMDGFKNPNEGVIIG GATNFPALDNALIRPGRFDMQVT VPRPDVKGRTEILKWYLNKIKFDQSVDPETIARG TVGFSGAELENLVNQAALKAADV KEMVTMKELEFSKDKILMGPERRSVEIDNKNKTI TAYHESGHAI IAYYTKDAMPINKA TIMPRGPTLGHVSLLPENDRWNETRAQLLAQMDV SMGGRVAEELIFGTDHITTGASSD FDNATKIAKRMVTKFGMSEKLGVMYTSYDTGKLSP ETQSAIEQEIRILLRDSYERAKHI LKTHAKEHKNLAEALLTYETLDAKEIQIVLEGKK LEVR"
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repeat-region	138595..138907	/note="AluSq repeat: matches 1..312 of consensus"
repeat-region	138928..139041	/note="FLAM-A repeat: matches 1..127 of consensus"
repeat-region	139094..139173	/note="AluSg/x repeat: matches 217..299 of consensus"
repeat-region	139297..139442	/note="L1PB2 repeat: matches 6015..6155 of consensus"
repeat-region	139952..140253	/note="AluSx repeat: matches 1..303 of consensus"
repeat-region	140284..140479	/note="AluSg/x repeat: matches

repeat-region	140530..140820	115..303 of consensus" /note="AluJo repeat: matches 1..298 of consensus"
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repeat-region	146265..146567	/note="L1MB7 repeat: matches 5823..6171 of consensus"
repeat-region	146733..146909	/note="AluJo repeat: matches 118..298 of consensus"
repeat-region	146927..146954	/note="AluSg1 repeat: matches 102..129 of consensus"
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repeat-region	150312..150486	/note="L1ME repeat: matches 5613..5799 of consensus"
repeat-region	150516..150847	/note="L1MC4 repeat: matches 7418..7786 of consensus"
repeat-region	150848..151180	/note="AluSx repeat: matches 3..298 of consensus"
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repeat-region	151367..151612	/note="AluJb repeat: matches 1..260 of consensus"
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153901	aggagatcaa	gaccagcctg	ggcaacgcag	ctaaatcccg	actctacaaa	aaaaaactac
153961	aaaaattagc	caggcatagg	ggcacacgcc	tgtagtccta	gctacctgag	aggctgaggc
154021	gggaggatgg	ctggagccca	ggaggaggag	gttggttgta	gctaagatca	cactactgca
154081	cttcagtctg	ggtgatagag	ccagaccctg	tctagaaaga	ataataaaa	taaattaaaa
154141	aattagccaa	gtgtggtggt	gcatgcctgt	ggtctcagct	acaagggagg	ttaaggcagg
154201	agtatcactt	gagcccagaa	ggtcaaagct	gcagtgagcc	atgatcatgc	cactgcactc
154261	cagcctgggc	aagagagcaa	gaccctgtct	caaaaaaaaa	aaaaaaaaaa	aaaaaaaaac
154321	tctcattcca	aaagaagtgt	gatatatcca	gtaagtatgt	aagtacatta	cagacagaga
154381	ataacaatgc	tgtgtctgac	ctcagcctta	atacaggctc	aatttagaaa	aggcatgcag
154441	acctcaaaca	caatgagaag	ggccctccac	gctgatgact	gaagttttca	aataatcact
154501	gcaccaacct	cttcctcaat	tgttcccttt	atacaattcc	aacagggttc	atagccattt
154561	aaactggaaa	ggaaaggaaa	gaactacttg	gttgtaaaac	tatcataatg	attcccaatg
154621	ccttattccc	caatagtcaa	ggctgaaaaa	acatggttat	gtataaacag	agacacgaat
154681	aagtaaagaa	gaaaagcaga	aataataaca	taaccaatct	cttcagagtt	ggaagagtcc
154741	tcagatcacg	tacttcaaat	ccctcctgcg	gaagaatttc	ttctaaaaca	ctcctgaaag
154801	ataattaccc	agccactaca	gttctgagaa	atcaaagtga	atagagcaga	tataatggca
154861	aagcacagag	aagagcacag	tgtggtacta	aagttgcaga	attc	

=>

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LOCUS (LOC): AL157387 GenBank (R)
GenBank ACC. NO. (GBN): AL157387
GenBank VERSION (VER): AL157387.9 GI:14787431
CAS REGISTRY NO. (RN): 256612-38-1
SEQUENCE LENGTH (SQL): 149730
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Primates
DATE (DATE): 13 Jul 2001
DEFINITION (DEF): Human DNA sequence from clone RP11-20F24 on chromosome
10p11.21-12.1, complete sequence.
SOURCE:
ORGANISM (ORGN): Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
Hominidae; Homo
NUCLEIC ACID COUNT (NA): 43347 a 27477 c 28670 g 50236 t
COMMENT:

On Jul 17, 2001 this sequence version replaced gi:14669197.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr10>

RP11-20F24 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone
RP11-20F24 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP11-20F24 is at 1 in this sequence. The
true left end of clone CTB-BR164I22 is at 147731 in this sequence.
The true right end of clone RP11-739D18 is at 62378 in this
sequence. The true right end of clone RP13-263N18 is at 119767 in
this sequence.

REFERENCE: 1 (bases 1 to 149730)
AUTHOR (AU): Clark, S.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (13-JUL-2001) Sanger Centre, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests:
clonerequest@sanger.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..149730	/organism="Homo sapiens" /db-xref="taxon:9606" /chromosome="10" /map="p11.21-12.1" /clone="RP11-20F24" /clone-lib="RPCI-11.1"
misc-feature	2833..2940	/note="match: STS: Em:G34561"
repeat-region	2979..3018	/note="20 copies 2 mer at 100% conserved"
repeat-region	3762..3937	/note="L2 repeat: matches 2164..2346 of consensus"
repeat-region	5075..5595	/note="L1MB8 repeat: matches 5653..6171 of consensus"
repeat-region	6189..6246	/note="MER47 repeat: matches 2260..2317 of consensus"
repeat-region	6283..6330	/note="24 copies 2 mer aa 72% conserved"
repeat-region	8791..9085	/note="L1MB8 repeat: matches 5860..6173 of consensus"
repeat-region	9106..9407	/note="L1PA5 repeat: matches 5846..6145 of consensus"
repeat-region	9408..9463	/note="L1P repeat: matches 2191..2256 of consensus"
repeat-region	9469..10500	/note="L1MB8 repeat: matches 4771..5874 of consensus"
repeat-region	11862..11989	/note="MLT1H repeat: matches 406..534 of consensus"
repeat-region	12348..12597	/note="L1MA5 repeat: matches 6048..6295 of consensus"
repeat-region	12775..12995	/note="L1MA3 repeat: matches 6104..6304 of consensus"
repeat-region	14143..14201	/note="L1MA9 repeat: matches 6213..6271 of consensus"
repeat-region	15645..15704	/note="3 copies 20 mer 85% conserved"
repeat-region	15755..15906	/note="FAM repeat: matches -108..48 of consensus"
repeat-region	17483..17537	/note="L2 repeat: matches 2649..2703 of consensus"
repeat-region	17835..17914	/note="4 copies 20 mer 95% conserved"
repeat-region	18751..19057	/note="AluY repeat: matches 1..308 of consensus"
repeat-region	21334..21455	/note="L1PA4 repeat: matches 6025..6146 of consensus"
repeat-region	24873..25082	/note="L1MC4 repeat: matches 7614..7837 of consensus"
repeat-region	25195..25481	/note="L1MC4 repeat: matches 7167..7465 of consensus"
repeat-region	25582..26124	/note="TIGGER2 repeat: matches 80..689 of consensus"
repeat-region	26125..26432	/note="AluY repeat: matches 2..299 of consensus"
repeat-region	26433..26517	/note="TIGGER2 repeat: matches 1..80 of consensus"
repeat-region	26519..26554	/note="L1MC4 repeat: matches 6486..6525 of consensus"
repeat-region	26572..27159	/note="MER6A repeat: matches 275..604 of consensus"
repeat-region	27268..27506	/note="MER6A repeat: matches 2..261 of consensus"
repeat-region	28089..28477	/note="L1M4 repeat: matches

repeat-region	28562..28876	4077..4501 of consensus" /note="MLT1E repeat: matches 249..568 of consensus"
repeat-region	29161..29437	/note="L1M4 repeat: matches 3711..3986 of consensus"
repeat-region	29732..29904	/note="MER20 repeat: matches 48..217 of consensus"
repeat-region	29931..30008	/note="AluS repeat: matches 3..80 of consensus"
repeat-region	30495..30579	/note="L1PA13 repeat: matches 5951..6037 of consensus"
repeat-region	30580..30895	/note="AluY repeat: matches 1..305 of consensus"
repeat-region	30896..31022	/note="L1PA13 repeat: matches 6037..6156 of consensus"
repeat-region	33510..33874	/note="MLT1A1 repeat: matches 1..365 of consensus"
repeat-region	35684..35849	/note="MIR repeat: matches 74..252 of consensus"
repeat-region	36196..36319	/note="MER3 repeat: matches 3..137 of consensus"
repeat-region	36321..36628	/note="L1MB8 repeat: matches 5858..6173 of consensus"
repeat-region	36629..36937	/note="AluY repeat: matches 3..309 of consensus"
repeat-region	36938..37663	/note="L1MB8 repeat: matches 5201..5858 of consensus"
repeat-region	37664..37971	/note="AluY repeat: matches 1..309 of consensus"
repeat-region	37972..38146	/note="L1MB8 repeat: matches 5023..5201 of consensus"
repeat-region	38147..38410	/note="L1PB3 repeat: matches 5881..6150 of consensus"
repeat-region	38454..38653	/note="L1MB4 repeat: matches 5980..6179 of consensus"
repeat-region	38655..38738	/note="MER3 repeat: matches 119..209 of consensus"
repeat-region	38825..38959	/note="L2 repeat: matches 2103..2238 of consensus"
repeat-region	39093..39246	/note="L2 repeat: matches 2404..2565 of consensus"
repeat-region	39256..39414	/note="FRAM repeat: matches -3..155 of consensus"
repeat-region	39744..40732	/note="L1P repeat: matches 2808..3792 of consensus"
repeat-region	40751..41122	/note="L1PA8 repeat: matches 5788..6159 of consensus"
repeat-region	41226..41671	/note="L1ME3 repeat: matches 4580..5044 of consensus"
repeat-region	41672..41975	/note="AluY repeat: matches 1..304 of consensus"
repeat-region	41976..42236	/note="L1ME3 repeat: matches 5044..5299 of consensus"
repeat-region	42274..42776	/note="L1ME3 repeat: matches 5408..5942 of consensus"
repeat-region	43018..43121	/note="L1MC4 repeat: matches 7872..7977 of consensus"
repeat-region	43124..43161	/note="19 copies 2 mer aa 78% conserved"
repeat-region	43791..44041	/note="L1PA16 repeat: matches 5896..6157 of consensus"
repeat-region	46248..46796	/note="MER1A repeat: matches 1..526 of consensus"
repeat-region	46800..46979	/note="L2 repeat: matches

repeat-region	49569..49605	1902..2072 of consensus"
		/note="tRNA-Met-i repeat: matches
repeat-region	49616..49918	1..37 of consensus"
		/note="AluSx repeat: matches
repeat-region	49954..50249	7..309 of consensus"
		/note="AluSq repeat: matches
repeat-region	50423..50716	1..301 of consensus"
		/note="AluSq repeat: matches
misc-feature	51798..51931	1..294 of consensus"
misc-feature	complement(51817..51929	/note="match: STS: Em:AU025697"
)	/note="match: STS: Em:AU049189"
misc-feature	51840..51932	
misc-feature	complement(51842..51947	/note="match: STS: Em:AU025554"
)	/note="match: STS: Em:G12353"
misc-feature	complement(51844..51947	
)	/note="match: STS: Em:AU027478"
misc-feature	complement(51846..51954	
)	/note="match: STS: Em:AU027419"
misc-feature	complement(51848..51940	
)	/note="match: STS: Em:AU047816"
misc-feature	51848..51945	
misc-feature	51848..51935	/note="match: STS: Em:AU048719"
repeat-region	51888..51925	/note="match: STS: Em:AU027904"
		/note="19 copies 2 mer ac 100%
		conserved"
repeat-region	51927..52033	/note="MER5A repeat: matches
		70..178 of consensus"
repeat-region	54525..56971	/note="L1P3 repeat: matches
		3178..5622 of consensus"
repeat-region	56967..57410	/note="L1P2 repeat: matches
		5333..5776 of consensus"
repeat-region	57411..58125	/note="LTR12 repeat: matches
		1..671 of consensus"
repeat-region	58126..60851	/note="HERV9 repeat: matches
		531..8399 of consensus"
repeat-region	60852..68695	/note="HERV9 repeat: matches
		17..2438 of consensus"
repeat-region	68701..69241	/note="L1M repeat: matches
		4807..5336 of consensus"
repeat-region	69240..72010	/note="L1P3 repeat: matches
		537..3184 of consensus"
repeat-region	72011..72213	/note="L1P3 repeat: matches 3..205
		of consensus"
repeat-region	72821..73229	/note="MER83 repeat: matches
		1..448 of consensus"
repeat-region	73285..73530	/note="L1ME2 repeat: matches
		5904..6152 of consensus"
repeat-region	75962..76256	/note="AluSg repeat: matches
		1..295 of consensus"
repeat-region	77376..77411	/note="18 copies 2 mer ct 94%
		conserved"
repeat-region	77412..77439	/note="14 copies 2 mer ca 100%
		conserved"
repeat-region	78284..78668	/note="L2 repeat: matches
		2006..2374 of consensus"
repeat-region	78685..79097	/note="MER72 repeat: matches
		230..668 of consensus"
repeat-region	79269..79406	/note="MER49 repeat: matches
		8..144 of consensus"
repeat-region	79416..79533	/note="L2 repeat: matches
		1809..1928 of consensus"
repeat-region	79774..79870	/note="Tigger3(Golem) repeat:
		matches 2938..3037 of consensus"
repeat-region	80431..80688	/note="7SLRNA repeat: matches

repeat-region	80711..80750	54..308 of consensus" /note="20 copies 2 mer tg 100% conserved"
repeat-region	80768..80903	/note="MIR repeat: matches 25..173 of consensus"
repeat-region	81555..81588	/note="17 copies 2 mer ag 85% conserved"
repeat-region	81971..82134	/note="MIR repeat: matches 2..174 of consensus"
repeat-region	83986..84129	/note="MIR repeat: matches 86..240 of consensus"
repeat-region	84166..84518	/note="MLT1A2 repeat: matches 1..361 of consensus"
repeat-region	85991..86091	/note="HY1 repeat: matches 10..112 of consensus"
repeat-region	86227..86901	/note="L1ME3 repeat: matches 5456..6148 of consensus"
repeat-region	87657..87957	/note="AluJo repeat: matches 1..281 of consensus"
repeat-region	88707..88832	/note="63 copies 2 mer aa 69% conserved"
repeat-region	88709..88808	/note="5 copies 20 mer 75% conserved"
repeat-region	89437..89482	/note="L1MA4A repeat: matches 6248..6294 of consensus"
repeat-region	90235..90377	/note="L1ME3A repeat: matches 5679..5830 of consensus"
repeat-region	92370..92548	/note="AluJo repeat: matches 121..305 of consensus"
repeat-region	93162..93455	/note="AluSx repeat: matches 1..295 of consensus"
repeat-region	94810..95119	/note="AluSg repeat: matches 1..309 of consensus"
repeat-region	95281..95310	/note="15 copies 2 mer tt 90% conserved"
repeat-region	95854..96166	/note="AluSx repeat: matches 1..312 of consensus"
repeat-region	99114..99695	/note="LTR14 repeat: matches 1..548 of consensus"
repeat-region	100979..101163	/note="MLT1D repeat: matches 253..430 of consensus"
repeat-region	101265..101427	/note="MLT1D repeat: matches 82..242 of consensus"
repeat-region	102566..102916	/note="L1PA13 repeat: matches 5791..6151 of consensus"
repeat-region	103158..103464	/note="AluSp repeat: matches 2..299 of consensus"
repeat-region	103466..103747	/note="AluSq repeat: matches 1..282 of consensus"
repeat-region	103760..104380	/note="LTR9 repeat: matches 10..609 of consensus"
repeat-region	104238..104399	/note="LTR25 repeat: matches 625..790 of consensus"
repeat-region	104408..104546	/note="HUIERS-P3 repeat: matches 15..155 of consensus"
repeat-region	104551..105818	/note="HUIERS-P3 repeat: matches 133..1400 of consensus"
repeat-region	105819..106121	/note="AluY repeat: matches 1..304 of consensus"
repeat-region	106122..107985	/note="HUIERS-P3 repeat: matches 1400..3334 of consensus"
repeat-region	107986..108221	/note="AluYb8 repeat: matches 72..307 of consensus"
repeat-region	108222..108497	/note="HUIERS-P3 repeat: matches

repeat-region	108498..108711	3334..3609 of consensus" /note="HUERS-P3 repeat: matches 6016..6236 of consensus"
repeat-region	108715..109007	/note="LTR9 repeat: matches 298..595 of consensus"
repeat-region	108886..109029	/note="LTR25 repeat: matches 642..781 of consensus"
repeat-region	109038..109176	/note="L2 repeat: matches 2144..2289 of consensus"
repeat-region	109731..110241	/note="MER9 repeat: matches 1..511 of consensus"
repeat-region	110595..110818	/note="L1P repeat: matches 1696..1923 of consensus"
repeat-region	110818..111347	/note="L1M1 repeat: matches 1918..2792 of consensus"
repeat-region	111309..111367	/note="L1 repeat: matches 2375..2433 of consensus"
repeat-region	111388..113527	/note="L1PB2 repeat: matches 2377..4531 of consensus"
repeat-region	113528..113851	/note="THE1C repeat: matches 1..317 of consensus"
repeat-region	113859..114058	/note="10 copies 20 mer 67% conserved"
repeat-region	113946..114097	/note="76 copies 2 mer ta 63% conserved"
repeat-region	114162..115573	/note="L1PB2 repeat: matches 4542..5978 of consensus"
repeat-region	115582..115726	/note="L1P5 repeat: matches 5254..5409 of consensus"
repeat-region	115734..115882	/note="L1PB2 repeat: matches 6002..6155 of consensus"
repeat-region	116377..117190	/note="L1MA4A repeat: matches 5463..6299 of consensus"
repeat-region	117187..117651	/note="L1PA3 repeat: matches 5683..6146 of consensus"
repeat-region	117655..118732	/note="L1MA4A repeat: matches 4401..5402 of consensus"
repeat-region	118733..119041	/note="AluSx repeat: matches 1..311 of consensus"
repeat-region	119042..120349	/note="L1MA4A repeat: matches 2930..4401 of consensus"
repeat-region	120374..120405	/note="L1PA6 repeat: matches 5896..5927 of consensus"
misc-feature	complement(122234..122472)	/note="match: STS: Em:HSJ16C7"
repeat-region	122985..123058	/note="37 copies 2 mer tt 64% conserved"
repeat-region	123065..123357	/note="AluY repeat: matches 3..295 of consensus"
repeat-region	123405..123983	/note="L1 repeat: matches 2118..2703 of consensus"
repeat-region	123912..124177	/note="L1M2 repeat: matches 1909..2569 of consensus"
repeat-region	124188..124942	/note="L1 repeat: matches 2124..2920 of consensus"
repeat-region	124872..125993	/note="L1M2 repeat: matches 1078..2572 of consensus"
repeat-region	125987..126124	/note="L1MA10 repeat: matches 6177..6312 of consensus"
repeat-region	126148..126647	/note="MLT1H repeat: matches 70..540 of consensus"
repeat-region	126655..126751	/note="MLT1H-internal repeat: matches 1..102 of consensus"
repeat-region	126836..126920	/note="L1M2 repeat: matches

repeat-region	126921..127219	1039..1123 of consensus"
		/note="AluY repeat: matches 2..296
repeat-region	127220..128278	of consensus"
		/note="L1M2 repeat: matches
repeat-region	128594..129049	-18..1039 of consensus"
		/note="L1M2 repeat: matches
repeat-region	129055..129272	-669..-215 of consensus"
		/note="L1 repeat: matches
repeat-region	129313..129728	4075..4318 of consensus"
		/note="L1PA7 repeat: matches
repeat-region	130852..131036	5726..6145 of consensus"
		/note="MLT1D repeat: matches
repeat-region	133038..133185	3..175 of consensus"
		/note="L1MEc repeat: matches
repeat-region	133219..133479	1550..1717 of consensus"
		/note="AluY repeat: matches
repeat-region	133482..133790	35..304 of consensus"
		/note="AluY repeat: matches 1..309
repeat-region	135210..135375	of consensus"
		/note="L1MA7 repeat: matches
repeat-region	135374..135964	5980..6141 of consensus"
		/note="L1MA4A repeat: matches
repeat-region	135973..136480	5681..6289 of consensus"
		/note="L1 repeat: matches
repeat-region	136481..137565	4174..4672 of consensus"
		/note="MER11C repeat: matches
repeat-region	137566..139412	2..1071 of consensus"
		/note="L1 repeat: matches
repeat-region	140679..140977	2279..4174 of consensus"
		/note="AluSq repeat: matches
repeat-region	141174..141731	6..299 of consensus"
		/note="L1 repeat: matches
repeat-region	141971..142326	3514..4090 of consensus"
		/note="L1MB5 repeat: matches
repeat-region	142350..143151	4472..4859 of consensus"
		/note="L1MB5 repeat: matches
repeat-region	143579..143971	5050..5884 of consensus"
		/note="L1PA16 repeat: matches
repeat-region	143996..145440	5658..6061 of consensus"
		/note="L1M1 repeat: matches
repeat-region	145585..145664	4089..5402 of consensus"
		/note="4 copies 20 mer 76%
repeat-region	145668..146304	conserved"
		/note="L1MA6 repeat: matches
repeat-region	146301..146649	5571..6294 of consensus"
		/note="L1M4 repeat: matches
repeat-region	146650..146957	4909..5254 of consensus"
		/note="AluY repeat: matches 1..298
repeat-region	146958..147995	of consensus"
		/note="L1M4 repeat: matches
repeat-region	147996..148296	3880..4909 of consensus"
		/note="AluY repeat: matches 1..291
repeat-region	148297..148666	of consensus"
		/note="L1M4 repeat: matches
repeat-region	148667..148959	3478..3880 of consensus"
		/note="AluY repeat: matches 1..292
repeat-region	148960..149175	of consensus"
		/note="L1M4 repeat: matches
repeat-region	149596..149730	3265..3478 of consensus"
		/note="MER2 repeat: matches 2..131
		of consensus"

SEQUENCE (SEQ):

1 gaattcagag ttctatgtta aaaatgcata ctatTTTTat tctttaatta aatattatat

61	tctgtcttgt	tctaaaagag	atttaaaatt	tggtgataaa	atatataata	atcaacaagg
121	tacgttttaa	gcattactca	aaaaagaaac	aaaaggcata	tgggataaca	gatatttagac
181	tctttaacct	aatctgagat	tttaatatata	aaattatttt	tagggataact	tgccatattt
241	tagaagtatg	aatattttatg	tctaacagat	ctgtaaactt	gttcataaaa	agtaatcagt
301	taactttaat	cagtcactttt	aatcagttaa	ctctaaataa	tctgtcctca	ttgaggagta
361	attttgactg	cgtgagattt	ttaaaaataa	attttcaact	tataaattta	ctggatagct
421	tccaatattc	ttttctataa	cagtcgttgc	agttaatagt	agcagaaact	ttctaactgg
481	aagatgttct	tttctcgcta	tttttcaagt	atgtatgtca	tttggagag	tttggagtaa
541	taaatagctg	agaactagga	agaaaaaaat	tcaagaatat	aggaatttta	ttggactaat
601	aacccaatat	aggaagaaat	agatctcaaa	atgaattcta	ttttctaaca	aaatgaattt
661	taagataagt	atgtttaatg	gcagattgac	tttaaaccac	gaagaagaga	agagaagaaa
721	tgccgatata	ttaaatgaaa	aaattagggg	agaattagga	agaatcgaag	agcagcatag
781	gaaagagtta	gaagtgaac	aacaacttga	acaggctctc	agaatacaag	atatagaatt
841	gaagagtgt	gaaagtaatt	tgaatcaggt	aaatcaatct	ctgataaaaa	ttttatattt
901	ctaactttat	ttcatcaata	ttacttttaa	tatccctttg	atttagtatg	tattattcag
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